

SEQUENCE LISTING

<110> Busfield, Samantha J.

<120> NOVEL MOLECULES OF THE
HERPESVIRUS-ENTRY-MEDIATOR-RELATED
PROTEIN FAMILY AND USES THEREOF

<130> MBIO98-061CP1

<150> US 09/146,950

<151> 1998-09-03

<160> 58

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1929

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (297)...(875)

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Met
1
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gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga 347
Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg
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acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc 395
Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro
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Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val
35 40 45
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ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag 491
Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu
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gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc 539
Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly
70 75 80
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acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa	587
Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln	
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atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg	635
Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg	
100 105 110	
aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc	683
Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val	
115 120 125	
cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc	731
Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser	
130 135 140 145	
ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc ctg	779
Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu	
150 155 160	
tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag	827
Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu	
165 170 175	
gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac ctc	875
Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp Leu	
180 185 190	
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ggggccctgg gagccagggg ggctccctga ggctgagtga acactgggag ctgcacctgc	995
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<210> 2
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 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> (1)...(38)

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08:30	Home	Breakfast	
09:00	Home	Get ready	
09:30	Home	Leave	
10:00	Home	Arrive	
10:30	Home	Breakfast	
11:00	Home	Get ready	
11:30	Home	Leave	
12:00	Home	Arrive	
12:30	Home	Breakfast	
13:00	Home	Get ready	
13:30	Home	Leave	
14:00	Home	Arrive	
14:30	Home	Breakfast	
15:00	Home	Get ready	
15:30	Home	Leave	
16:00	Home	Arrive	
16:30	Home	Breakfast	
17:00	Home	Get ready	
17:30	Home	Leave	
18:00	Home	Arrive	
18:30	Home	Breakfast	
19:00	Home	Get ready	
19:30	Home	Leave	
20:00	Home	Arrive	
20:30	Home	Breakfast	
21:00	Home	Get ready	
21:30	Home	Leave	
22:00	Home	Arrive	
22:30	Home	Breakfast	
23:00	Home	Get ready	
23:30	Home	Leave	
24:00	Home	Arrive	

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<221> CDS
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1				5					10					15		
aga	acc	gac	gtc	ttg	agg	ctg	gtg	ctg	tat	ctc	acc	ttc	ctg	gga	gcc	96
Arg	Thr	Asp	Val	Leu	Arg	Leu	Val	Leu	Tyr	Leu	Thr	Phe	Leu	Gly	Ala	
			20					25					30			
ccc	tgc	tac	gcc	cca	gct	ctg	ccg	tcc	tgc	aag	gag	gac	gag	tac	cca	144
Pro	Cys	Tyr	Ala	Pro	Ala	Leu	Pro	Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	
			35				40					45				
gtg	ggc	tcc	gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggg	tat	cgt	gtg	aag	192
Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	
	50					55					60					
gag	gcc	tgc	ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	240
Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	
	65				70					75					80	

ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	

caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	

agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	

gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	

agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	

gtg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	

gag gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac	576
Glu Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp	
180 185 190	

ctc	579
Leu	

<210> 4
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<400> 4

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35 40 45	
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala	
50 55 60	
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val	
65 70 75 80	
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His	
85 90 95	
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val	
100 105 110	
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro	
115 120 125	
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln	

130 135 140
 Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp Leu
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 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala
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 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30
 ccc tgc tac gcc cca gct 114
 Pro Cys Tyr Ala Pro Ala
 35

<210> 7
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 7
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 1 5 10 15
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
 20 25 30
 Val Cys

<210> 8
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 <212> PRT
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<400> 8

Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 9
 <211> 42
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 <213> Homo sapiens

<400> 9

Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1 5 10 15
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 20 25 30
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

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 1 5 10 15

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc 96
 Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly
 20 25 30

aca gtg tgt 105
 Thr Val Cys
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 1 5 10 15
 ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
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 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
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 gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
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 gga ggc acc gag agt cag gac acc ctg tgt 126
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
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 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 -5 1 5 10
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro

ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag	488
Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu	
50 55 60 65	
gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc	536
Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly	
70 75 80	
acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa	584
Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln	
85 90 95	
atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg	632
Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg	
100 105 110	
aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc	680
Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val	
115 120 125	
cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc	728
Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser	
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Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu	
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Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu	
165 170 175	
gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc gga	872
Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly	
180 185 190	
gct ggg acc agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg agc	920
Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser	
195 200 205	
ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt gtg	968
Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val	
210 215 220 225	
aaa aga aga aag cca agg ggt gat gta gtc aag gtg atc gtc tcc gtc	1016
Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser Val	
230 235 240	
cag cgg aaa aga cag gag gca gaa ggt gag gcc aca gtc att gag gcc	1064
Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu Ala	
245 250 255	
ctg cag gcc cct ccg gac gtc acc acg gtg gcc gtg gag gag aca ata	1112
Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr Ile	
260 265 270	

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Pro Ser Phe Thr Gly Arg Ser Pro Asn His
275 280

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aaaaaaaaa aaaaaaaaaa aa 1724

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<400> 15
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Met Glu Pro
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cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac 163
Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp
5 10 15

gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc ccc tgc tac 211
Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr
20 25 30 35

gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc 259
Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser
40 45 50

gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc	307
Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys	
55 60 65	
ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac	355
Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr	
70 75 80	
att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt	403
Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys	
85 90 95	
gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag	451
Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu	
100 105 110 115	
aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac	499
Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp	
120 125 130	
ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc	547
Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly	
135 140 145	
cag agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag	595
Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln	
150 155 160	
aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt	643
Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys	
165 170 175	
cag cac cag acc aat tgg cct aat cat atg tgt gaa aag aag aaa gcc	691
Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala	
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Lys Gly	

307
355
403
451
499
547
595
643
691
747

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<210> 18
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 <222> (1)...(38)

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 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 -5 1 5 10
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 30 35 40
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 45 50 55
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 60 65 70
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 75 80 85 90
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 95 100 105
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 110 115 120
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
 125 130 135
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 140 145 150
 Lys Lys Ala Lys Gly
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 <222> (1)...(591)

<400> 19

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15
 aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc 96
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30
 ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca 144
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro

35	40	45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag			192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys			
50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca			240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro			
65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc			288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys			
85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc			336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser			
100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc			384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile			
115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc			432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser			
130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc			480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr			
145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg			528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu			
165	170	175	
gag gaa tgt cag cac cag acc aat tgg cct aat cat atg tgt gaa aag			576
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys			
180	185	190	
aag aaa gcc aag ggg			591
Lys Lys Ala Lys Gly			
195			

<210> 20
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 20
 Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys
 1 5 10 15
 Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
 20 25 30
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
 35 40 45
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
 50 55 60

Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
65 70 75 80
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
85 90 95
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
100 105 110
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
115 120 125
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
130 135 140
Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala Lys Gly
145 150 155

<210> 21
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> (1)...(38)

<400> 21

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-35 -30 -25
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala
-5

<210> 22
<211> 114
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(114)

<400> 22

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
1 5 10 15
aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
20 25 30
ccc tgc tac gcc cca gct 114
Pro Cys Tyr Ala Pro Ala
35

<210> 23
<211> 34
<212> PRT
<213> Homo sapiens

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<400> 23
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
 1          5          10          15
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
      20          25          30
Val Cys

<210> 24
<211> 42
<212> PRT
<213> Homo sapiens

<400> 24
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1          5          10          15
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
      20          25          30
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
      35          40

<210> 25
<211> 42
<212> PRT
<213> Homo sapiens

<400> 25
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1          5          10          15
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
      20          25          30
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
      35          40

<210> 26
<211> 105
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(105)

<400> 26
tcc tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag      48
Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys
 1          5          10          15

tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc      96
Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly
      20          25          30

aca gtg tgt      105
Thr Val Cys
      35

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<210> 27
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(126)

<400> 27

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 28
 <211> 126
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(126)

<400> 28

tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc	48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala	
1 5 10 15	

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
20 25 30	

gga ggc acc gag agt cag gac acc ctg tgt	126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys	
35 40	

<210> 29
 <211> 2313
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (85)...(642)

<400> 29

60
111
159
207
255
303
351
399
447
495
543
591
639
692
752
812
872
932

gtcgacccac gcgccggct gagttcctct gctggagttc atcctgctag ctgggttccc	60
gagctgccgg tctgagcctg aggc atg gag cct cct gga gac tgg ggg cct	111
Met Glu Pro Pro Gly Asp Trp Gly Pro	
1 5	
cct ccc tgg aga tcc acc ccc aga acc gac gtc tcg agg ctg gtg ctg	159
Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val Ser Arg Leu Val Leu	
10 15 20 25	
tat ctc acc ttc ctg gga gcc ccc tgc tac gcc cca gct ctg ccg tcc	207
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
30 35 40	
tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag tgc	255
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
45 50 55	
agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc aca	303
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
60 65 70	
gtg tgt gaa ccc tgc cct cca ggc acc tac att gcc cac ctc aat ggc	351
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
75 80 85	
cta agc aag tgt ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg	399
Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu	
90 95 100 105	
cgc gcg agc cgg aac tgc tcc agg aca gag aac gcc gtg tgt ggc tgc	447
Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys	
110 115 120	
agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc gcg	495
Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala	
125 130 135	
tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag gga	543
Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly	
140 145 150	
ggc acc gag agt cag gac acc ctg tgt cag aac tgc ccc ccg ggg acc	591
Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr	
155 160 165	
ttc tct ccc aat ggg acc ctg gag gaa tgt cag cac cag acc aaa aag	639
Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Lys	
170 175 180 185	
gct tgaagggtccc accctgagcg gcaccctggc cacatgcctg cgtccaggag	692
Ala	
agctgcaggg ctgaagcctg tgtgccccag ataaccctt ccatgggccc agacaaagcc	752
tcatcagatc tgagcttccct ggaggctcag gatgggcctt cccagaagca ggcccagagg	812
gaggctgcct ccagatcccc tgtcccctgg ggctgtgggt gtccctgaat gtcagggccca	872
tgggagggcc cctgggcttc aggggttggg gaaagtgaac actctgctct ttgtccacct	932

Glu Glu Cys Gln His Gln Thr Lys Lys Ala
 140 145

<210> 31
 <211> 558
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(558)

<400> 31

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15

aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30

ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca 144
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 35 40 45

gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag 192
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 50 55 60

gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca 240
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 65 70 75 80

ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc 288
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 85 90 95

caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc 336
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 100 105 110

agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc 384
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 115 120 125

gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc 432
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 130 135 140

agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc 480
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 145 150 155 160

ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg 528
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
 165 170 175

gag gaa tgt cag cac cag acc aaa aag gct
 Glu Glu Cys Gln His Gln Thr Lys Lys Ala
 180 185

<210> 32
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 32

Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys
 1 5 10 15
 Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu
 20 25 30
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His
 35 40 45
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala
 50 55 60
 Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val
 65 70 75 80
 Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His
 85 90 95
 Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val
 100 105 110
 Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro
 115 120 125
 Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln
 130 135 140
 Thr Lys Lys Ala
 145

<210> 33
 <211> 38
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(38)

<400> 33

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 -35 -30 -25
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10
 Pro Cys Tyr Ala Pro Ala
 -5

<210> 34
 <211> 114
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(114)

<400> 34
 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 1 5 10 15

aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 20 25 30

ccc tgc tac gcc cca gct 114
 Pro Cys Tyr Ala Pro Ala
 35

<210> 35
 <211> 34
 <212> PRT
 <213> Homo sapiens

<400> 35
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys
 1 5 10 15
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr
 20 25 30
 Val Cys

<210> 36
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 36
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1 5 10 15
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
 20 25 30
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
 35 40

<210> 37
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 37
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1 5 10 15
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
 20 25 30
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
 35 40

<210> 38
 <211> 105
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(105)

<400> 38

tcc	tgc	aag	gag	gac	gag	tac	cca	gtg	ggc	tcc	gag	tgc	tgc	ccc	aag	48
Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	
1			5					10						15		

tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	gcc	tgc	ggg	gag	ctg	acg	ggc	96
Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	
			20					25					30			

aca	gtg	tgt														105
Thr	Val	Cys														
			35													

<210> 39

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(126)

<400> 39

tgc	cct	cca	ggc	acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	48
Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	
1			5					10						15		

ctg	cag	tgc	caa	atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	96
Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	
			20					25					30			

aac	tgc	tcc	agg	aca	gag	aac	gcc	gtg	tgt							126
Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	Cys							
			35				40									

<210> 40

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(126)

<400> 40

tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	cag	gac	ggg	gac	cac	tgc	gcc	48
Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	Cys	Ala	
1			5					10						15		

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
20 25 30

gga ggc acc gag agt cag gac acc ctg tgt 126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
35 40

<210> 41
<211> 1834
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103)...(933)

<400> 41

gtcgaccac gcgtccgcac agccgcagca atggcgctga gttcctctgc tggagttcat 60
cctgctagct gggttcccga gctgccggtc tgagcctgag gc atg gag cct cct 114
Met Glu Pro Pro
1

gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac gtc 162
Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val
5 10 15 20

ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc tgc tac gcc 210
Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala
25 30 35

cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc gag 258
Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu
40 45 50

tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg 306
Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly
55 60 65

gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac att 354
Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile
70 75 80

gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt gac 402
Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp
85 90 95 100

cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag aac 450
Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn
105 110 115

gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg 498
Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly
120 125 130

gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag 546

Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln		
		135					140					145					
agg	gtg	cag	aag	gga	ggc	acc	gag	agt	cag	gac	acc	ctg	tgt	cag	aac		594
Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn		
	150					155					160						
tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	gaa	tgt	cag		642
Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln		
	165				170					175					180		
cac	cag	acc	aag	tgc	agc	tgg	ctg	gtg	acg	aag	gcc	gga	gct	ggg	acc		690
His	Gln	Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr		
			185						190					195			
agc	agc	tcc	cac	tgg	gta	tgg	tgg	ttt	ctc	tca	ggg	agc	ctc	gtc	atc		738
Ser	Ser	Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	Leu	Val	Ile		
			200					205					210				
gtc	att	ggt	tgc	tcc	aca	ggt	ggc	cta	atc	ata	tgt	gtg	aaa	aga	aga		786
Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val	Lys	Arg	Arg		
	215						220					225					
aag	cca	agg	ggt	gat	gta	gtc	aag	gtg	atc	gtc	tcc	gtc	cag	gta	ttg		834
Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val	Gln	Val	Leu		
	230					235					240						
atc	ctc	ctc	ccc	ctc	tcc	ctc	ccc	cct	cca	cct	tcc	cac	ctc	ccc	tct		882
Ile	Leu	Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	His	Leu	Pro	Ser		
	245				250					255					260		
ccc	cgc	tgg	ggc	tgg	tgt	ttc	tgg	tgt	aca	tgg	tgg	ggg	ctc	cca	gtt		930
Pro	Arg	Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	Gly	Leu	Pro	Val		
			265					270					275				
ctc	tgagggtcct	gagtcctttca	agtacagcca	cggtagctca	ggaaagaacc												983
Leu																	
cacccccctca	aactgaaagc	agtaaaatga	acccgagaaac	ctggagtcctc	agggggggcct												1043
gagcaggcag	ggtctccacg	attcgtgtgc	tcacagcgga	aaagacagga	ggcagaaggt												1103
gaggccacag	tcattgaggc	cctgcaggcc	cctccggacg	tcaccacggt	ggccgtggag												1163
gagacaatac	cctcattcac	ggggaggagc	ccaaaccact	gacccacaga	ctctgcaccc												1223
cgacgccaga	gatacctgga	gcgacggctg	ctgaaagagg	ctgtccacct	ggcgaaacca												1283
ccggagcccg	gaggcttggg	ggctccgccc	tgggctggct	tccgtctcct	ccagtggagg												1343
gagaggtggg	gcccctgctg	gggtagagct	ggggacgcca	cgtgccattc	ccatggggcca												1403
gtgagggcct	ggggcctctg	ttctgctgtg	gcctgagctc	cccagagtcc	tgaggaggag												1463
cgccagtgtg	ccctcgctca	cagaccacac	acccagccct	cctggggccag	cccagagggc												1523
ccttcagacc	ccagctgtct	gcgcgtctga	ctcttgctggc	ctcagcagga	caggccccgg												1583
gcactgcctc	acagccaagg	ctggactggg	ttggctgcag	tgtggtgttt	agtggatacc												1643
acatcggaag	tgattttcta	aattggatgt	gaattcggct	cctgttttct	atttgtcatg												1703
aaacagtgtg	tttgggggaga	tgctgtggga	ggatgtaaat	atcttggttc	tcctcaaaaa												1763
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa												1823
agggcgcccg	c																1834

<210> 42
<211> 277

<212> PRT
 <213> Homo sapiens

<220>
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 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 30 35 40
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 45 50 55
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 60 65 70
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 75 80 85 90
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 95 100 105
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 110 115 120
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
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 Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
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 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
 175 180 185
 Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
 190 195 200
 Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Ser
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Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	20	25	30	
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Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca				240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc				288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc				336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc				384
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Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc				480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg				528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	165	170	175	
gag gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc				576
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala	180	185	190	
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Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly	195	200	205	
agc ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt				672
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys	210	215	220	
gtg aaa aga aga aag cca agg ggt gat gta gtc aag gtg atc gtc tcc				720
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser	225	230	235	240

gtc	cag	gta	ttg	atc	ctc	ctc	ccc	ctc	tcc	ctc	ccc	cct	cca	cct	tcc	768
Val	Gln	Val	Leu	Ile	Leu	Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	
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cac	ctc	ccc	tct	ccc	cgc	tgg	ggc	tgg	tgt	ttc	tgg	tgt	aca	tgg	tgg	816
His	Leu	Pro	Ser	Pro	Arg	Trp	Gly	Trp	Cys	Phe	Trp	Cys	Thr	Trp	Trp	
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Gly	Leu	Pro	Val	Leu												
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Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	
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Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	
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Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	
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Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	
				85					90					95		
Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	
			100					105					110			
Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	Cys	Gln	Asn	Cys	Pro	
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Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	Glu	Cys	Gln	His	Gln	
	130					135					140					
Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	Ala	Gly	Thr	Ser	Ser	
145					150					155					160	
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				165				170						175		
Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val	Lys	Arg	Arg	Lys	Pro	
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Leu	Pro	Leu	Ser	Leu	Pro	Pro	Pro	Pro	Ser	His	Leu	Pro	Ser	Pro	Arg	
	210					215					220					
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Pro Cys Tyr Ala Pro Ala
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29

Thr Val Cys
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Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	
			20					25					30			

aac	tgc	tcc	agg	aca	gag	aac	gcc	gtg	tgt							126
Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	Cys							
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1				5					10					15		

gcg	tgc	cgc	gct	tac	gcc	acc	tcc	agc	ccg	ggc	cag	agg	gtg	cag	aag	96
Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	
			20					25					30			

gga	ggc	acc	gag	agt	cag	gac	acc	ctg	tgt							126
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5 10 15

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Input file T198sHVEML; Output File T198sHVEML.pat
Sequence length 1929

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CAGCTTGTACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGCAATGGCGCTGAGTT	237
CCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGC	311
ATG GAG CCT CCT GGA	5
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Y L T F L G A P C Y A P A L P S C K E D	45
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC	431
E Y P V G S E C C P K C S P G Y R V K E	65
GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG	491
A C G E L T G T V C E P C P P G T Y I A	85
GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC	551
H L N G L S K C L Q C Q M C D P A M G L	105
CAC CTC AAT GGC CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG	611
A S R N C S R T E N A V C G C S P G H	125
GCG GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC	671
C I V Q D G D H C A A C R A Y A T S S	145
TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC	731
G Q R V Q K G G T E S Q D T L C Q N C	165
CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC	791
P P G T F S P N G T L E E C Q H Q T N R	185
GCC CCG GGG ACC TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAC CGA	851
W K S Q T D L *	194
GCT TGG AAA AGT CAG ACA GAC CTC TGA	878
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Figure 1

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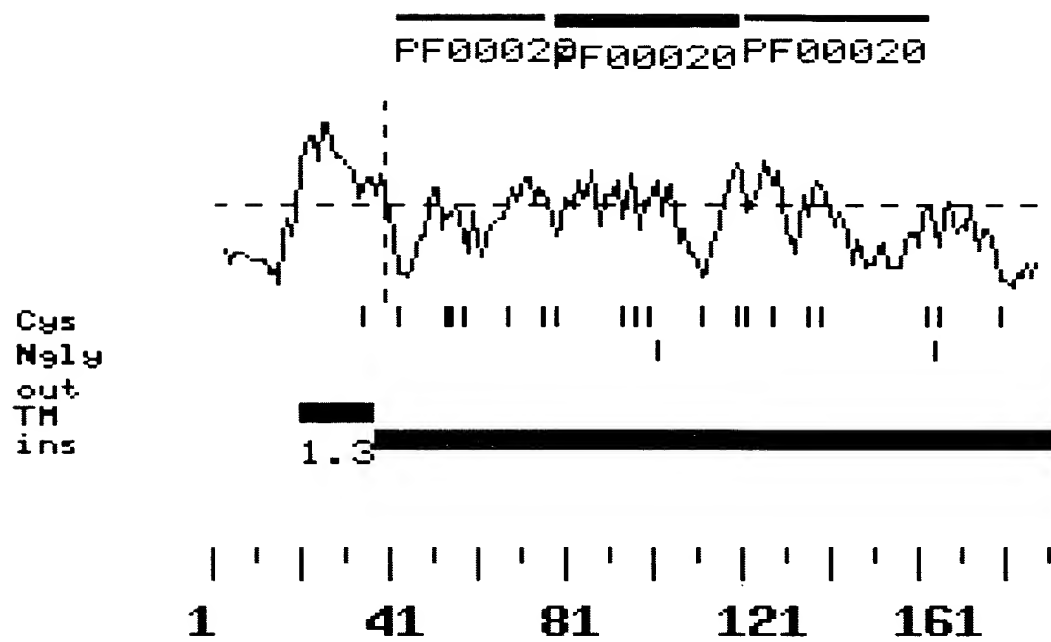


Figure 2

Input file T198sHVEM2; Output File T198sHVEM2.pat
Sequence length 1596

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S   T   P   R   T   D   V   L   R   L   V   L   Y   L   T   F   L   G   A   P   33
TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTT CTG GGA GCC CCC 205

C   Y   A   P   A   L   P   S   C   K   E   D   E   Y   P   V   G   S   E   C   53
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C   P   K   C   S   P   G   Y   R   V   K   E   A   C   G   E   L   T   G   T   73
TGC CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA 325

V   C   E   P   C   P   P   G   T   Y   I   A   H   L   N   G   L   S   K   C   93
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT 385

L   Q   C   Q   M   C   D   P   A   M   G   L   R   A   S   R   N   C   S   R   113
CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG 445

T   E   N   A   V   C   G   C   S   P   G   H   F   C   I   V   Q   D   G   D   133
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H   C   A   A   C   R   A   Y   A   T   S   S   P   G   Q   R   V   Q   K   G   153
CAG TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA 565

G   T   E   S   Q   D   T   L   C   Q   N   C   P   P   G   T   F   S   P   N   173
GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC TTC TCT CCC AAT 625

G   T   L   E   E   C   Q   H   Q   T   N   W   P   N   H   M   C   E   K   K   193
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K   A   K   G   *   198
AAA GCC AAG GGG TGA 700

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Figure 3

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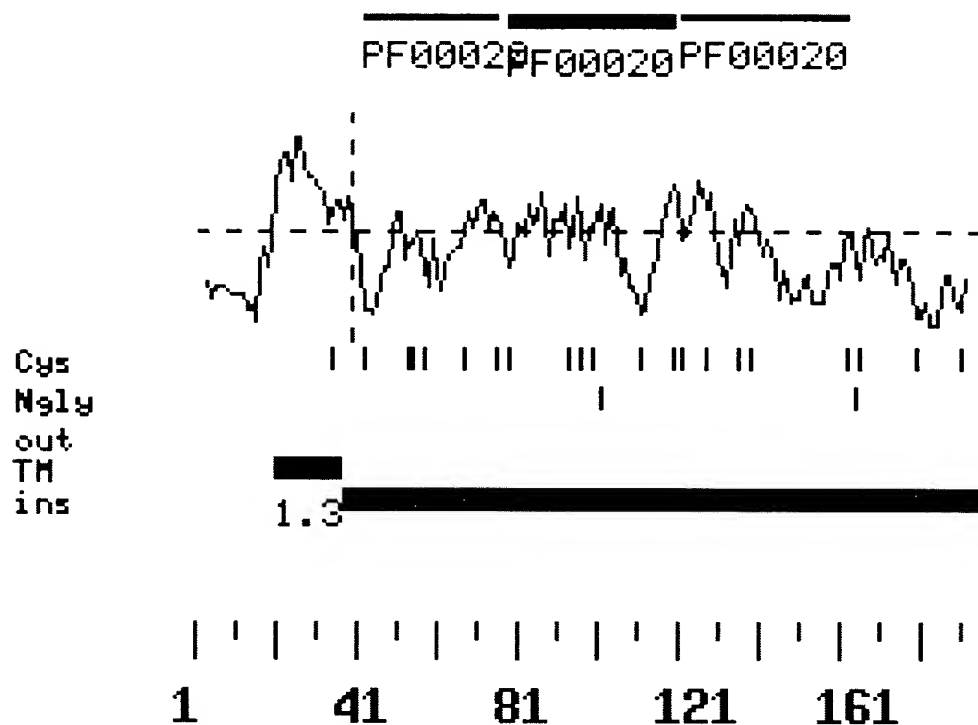


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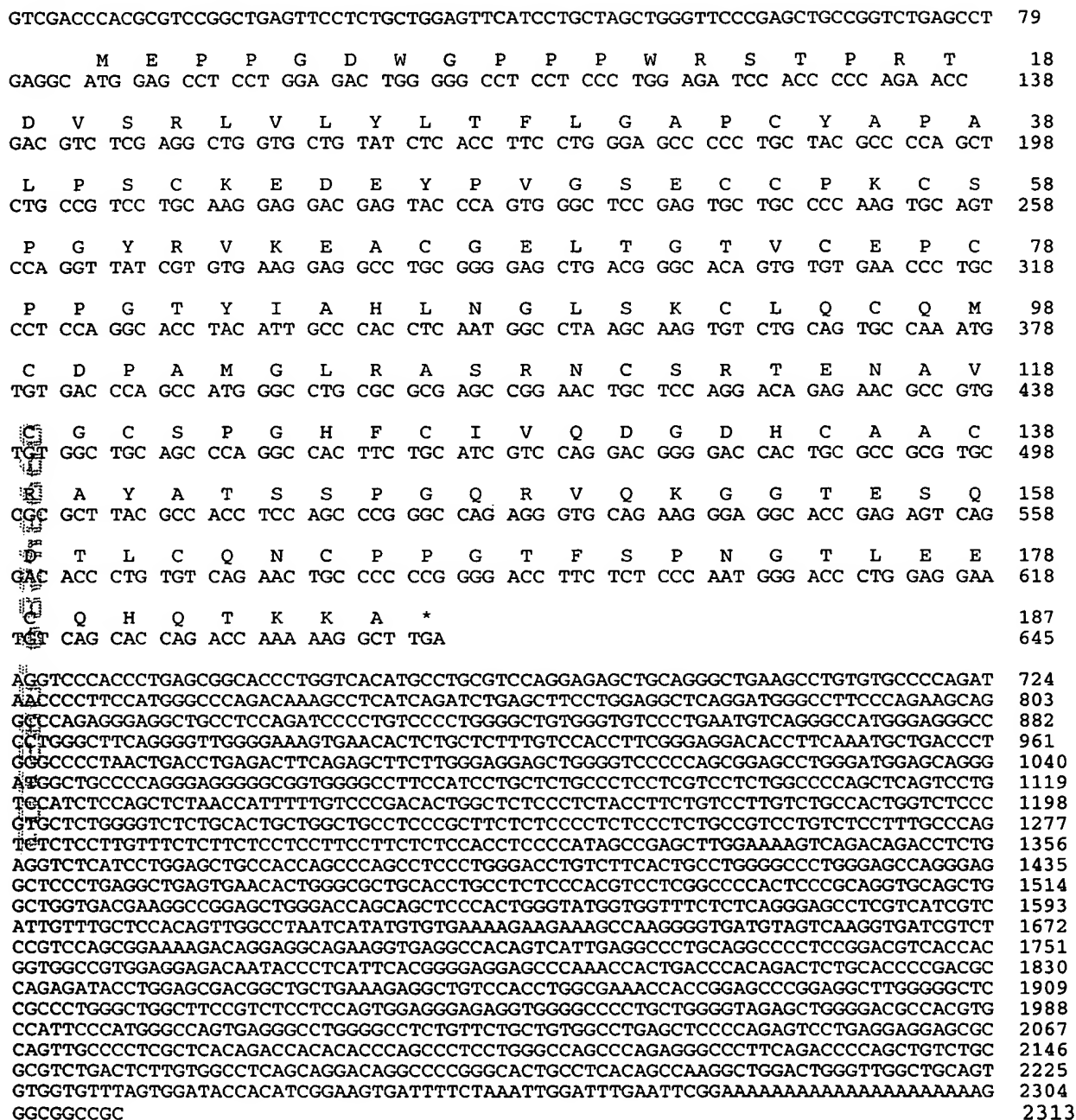


Figure 5

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ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC TTC CTG GGA GCC CCC TGC	204
Y A P A L P S C K E D E Y P V G S E C C	54
TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC	264
P K C S P G Y R V K E A C G E L T G T V	74
CCC AAG TGC AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG	324
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TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG TGT CTG	384
Q C Q M C D P A M G L R A S R N C S R T	114
CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC TCC AGG ACA	444
E N A V C G C S P G H F C I V Q D G D H	134
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A A C R A Y A T S S P G Q R V Q K G G	154
TGC GCC GCG TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC	564
E S Q D T L C Q N C P P G T F S P N G	174
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L E E C Q H Q T K C S W L V T K A G A	194
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K V I V S V Q V L I L L P L S L P P P	254
GTC AAG GTG ATC GTC TCC GTC CAG GTA TTG ATC CTC CTC CCC CTC TCC CTC CCC CCT CCA	864
P S H L P S P R W G W C F W C T W W G L	274
CCT TCC CAC CTC CCC TCT CCC CGC TGG GGC TGG TGT TTC TGG TGT ACA TGG TGG GGG CTC	924
P V L *	278
CCA GTT CTC TGA	936
GGTCTGAGTCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCCACCCCTCAAAGTCAAAGCAGTAAATGAAC	1015
CCGAGAACCTGGAGTCCCAGGGGGGCCCTGAGCAGGCAGGGTCTCCACGATTCGTGTGCTCACAGCGGAAAAGACAGGAG	1094
GCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAATAC	1173
CCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCT	1252
GCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCTC	1331
CTCCAGTGGAGGGAGAGGTGGGGCCCTGTCTGGGGTAGAGCTGGGGACGCCACGTGCCATTTCCCATGGGCCAGTGAGGG	1410
CCTGGGGCTCTGTTCTGTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTTCGCTCACAGACC	1489
ACACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAG	1568
CAGGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTGTTAGTGGATACACAT	1647
CGGAAGTGATTTTCTAAATTGGATTGTAATTCGGCTCCTGTTTTCTATTTGTGTCATGAAACAGTGTATTTGGGGAGATGC	1726
TGTGGGAGGATGTAATATCTTGTTCCTCAAA	1805
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGC	1834

Figure 7

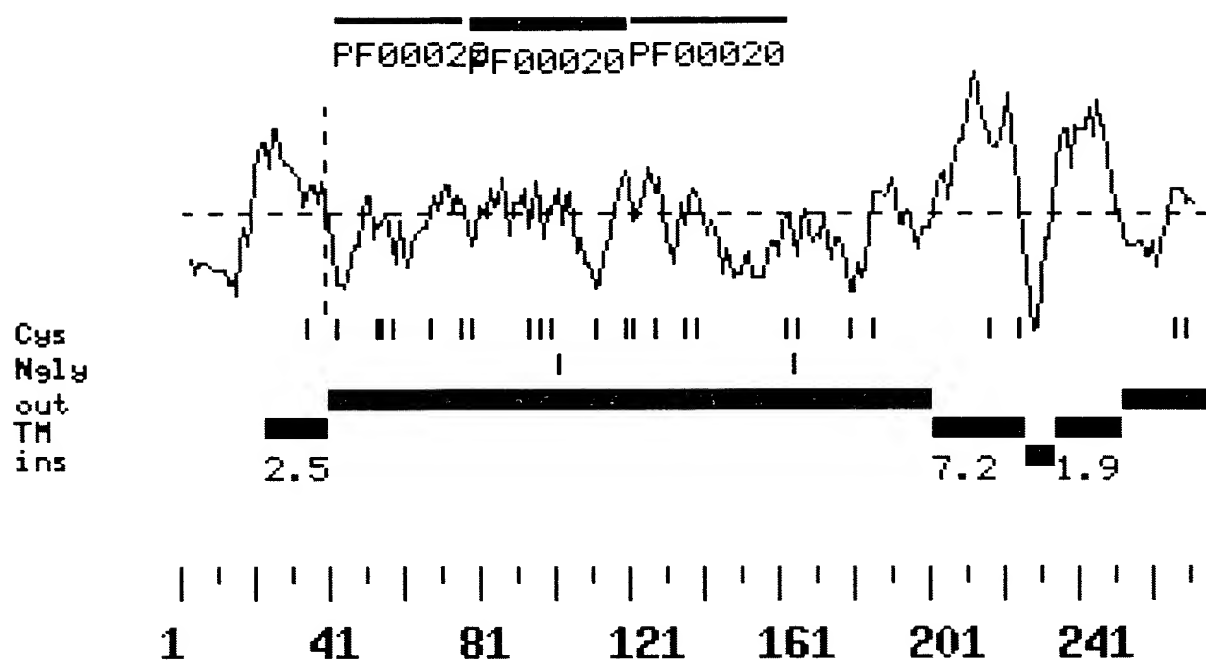


Figure 8

SHVEM_1_n.a.	1	80
SHVEM_2_n.a.	~GTCG-ACCCACGCGTCCGCTCGGCTTTGCCTGGACAGCTCCTGCCTCCCGCAGGGGCCACCTGTGTCCCCAGCGCCG	
SHVEM_3_n.a.	~GTCG-ACCCACGCGTCC-----GG-----ATG---A-----	
mHVEM_2_n.a.	~GTCG-ACCCACGCGTCC-----GC-----AC-----	
mHVEM__pub.__n.a.	CCTTCATACCGGCCCTTCCCCTCGGCTTTGCCTGGACAGCTCCTGCCTCCCGCAGGGGCCACCTGTGTCCCCAGCGCCG	
SHVEM_1_n.a.	81	160
SHVEM_2_n.a.	CTCCACCCAGCAGGCCCTGAGCCCCCTCTCTGCTGCCAGACACCCCTGCTGCCCACTCTCCTGTGCTCGGGTTCTGAGGC	
SHVEM_3_n.a.	-----AGGA-----	
mHVEM_2_n.a.	-----G-----	
mHVEM__pub.__n.a.	-----AG-----	
	CTCCACCCAGCAGGCCCTGAGCCCCCTCTCTGCTGCCAGACACCCCTGCTGCCCACTCTCCTGTGCTCGGGTTCTGAGGC	
SHVEM_1_n.a.	161	240
SHVEM_2_n.a.	ACAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCACAGCCGAGCAATGGCGCTGAGTT	
SHVEM_3_n.a.	-----CCGCAGCAATGGCGCTGAGTT	
mHVEM_2_n.a.	-----GCTGAGTT	
mHVEM__pub.__n.a.	-----CCGCAGCAATGGCGCTGAGTT	
	ACAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCT-----CTTCTGGCCACAGCCGAGCAATGGCGCTGAGTT	
SHVEM_1_n.a.	241	320
SHVEM_2_n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
SHVEM_3_n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
mHVEM_2_n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
mHVEM__pub.__n.a.	CCTCTGTGAGGTTTCATCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGG	
SHVEM_1_n.a.	321	400
SHVEM_2_n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCTGGGAGCCCCCTG	
SHVEM_3_n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCTGGGAGCCCCCTG	
mHVEM_2_n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCTGGGAGCCCCCTG	
mHVEM__pub.__n.a.	GGGCCTCCTCCCTGGAGATCCACCCCCAGAACCGACGCTTTGAGGCTGGTGCTGTATCTCACCTTCTGGGAGCCCCCTG	
SHVEM_1_n.a.	401	480
SHVEM_2_n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
SHVEM_3_n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
mHVEM_2_n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
mHVEM__pub.__n.a.	CTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTT	
SHVEM_1_n.a.	481	560
SHVEM_2_n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
SHVEM_3_n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
mHVEM_2_n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
mHVEM__pub.__n.a.	ATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCTGCCCTCCAGGCACCTACATTGCCACCTC	
SHVEM_1_n.a.	561	640
SHVEM_2_n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACGTCTCCAGGAC	
SHVEM_3_n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACGTCTCCAGGAC	
mHVEM_2_n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACGTCTCCAGGAC	
mHVEM__pub.__n.a.	AATGGCCTAAGCAAGTGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGGAGCCGGAACGTCTCCAGGAC	
SHVEM_1_n.a.	641	720
SHVEM_2_n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
SHVEM_3_n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
mHVEM_2_n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
mHVEM__pub.__n.a.	AGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTT	
SHVEM_1_n.a.	721	800
SHVEM_2_n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGAGAACTGCCCCCG	
SHVEM_3_n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGAGAACTGCCCCCG	
mHVEM_2_n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGAGAACTGCCCCCG	
mHVEM__pub.__n.a.	ACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCTGTGTGAGAACTGCCCCCG	

Figure 9A

SHVEM_1_n.a.	801	880
SHVEM_2_n.a.	GGGACCTTCTCTCCCAATGGGACCC	-----
SHVEM_3_n.a.	GGGACCTTCTCTCCCAATGGGACCC	GGGAGGAATGTCAGCACCAGACCAA
mHVEM_2_n.a.	GGGACCTTCTCTCCCAATGGGACCC	GGGAGGAATGTCAGCACCAGACCAA
mHVEM_pub._n.a.	GGGACCTTCTCTCCCAATGGGACCC	GGGAGGAATGTCAGCACCAGACCAA
SHVEM_1_n.a.	881	960
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	CCCTGGTCACATGCC	TGCCGTCAGGAGCTGCAGGGCTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCCAG
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	961	1040
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	CAAAGCCTCATCAGATCTGAGCTT	CTCCGAGGCTCAGGATGGGCCCTTCCAGAAGCAGGCCAGAGGGAGGCTGCCTCCA
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	1041	1120
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	GATCCCTGTCCCTTGGGGCTGTGGG	TGTCCTGAATGTCAGGGCCATGGGAGGGCCCTGGGCTTCAGGGGTGGGGAA
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	1121	1200
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	AGTGAACACTCTGCTCTTGTCCAC	CTTCGGGAGGACACCTTCAAATGCTGACCCTGGGCCCCTAAGTACCTGAGACTT
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	1201	1280
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	CAGAGCTTCTTGGGAGGAGCTGGGG	TCCCCAGCGGAGCCTGGGATGGAGCAGGGATGGCTGCCCCAGGGAGGGGGCGGT
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	1281	1360
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	GGGGCCTTCCATCCTGCTCTGCCCT	CTCGTCCTCTGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTTTG
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	1361	1440
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	TCCCGACACTGGCTCTCCCTCTAC	CTTCTGTCCTTGTCTGCCACTGGTCTCCCGTGTCTGGGGTCTCTGCACTGCTGGC
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----
SHVEM_1_n.a.	1441	1520
SHVEM_2_n.a.	-----	-----
SHVEM_3_n.a.	TGCCTCCCGCTTCTCTCCCTCTCC	CTCTGCCGTCTGTCTCCTTTGCCAGTCTCTCCTTGTTTCTCTCTCCTCTCTC
mHVEM_2_n.a.	-----	-----
mHVEM_pub._n.a.	-----	-----

Figure 9B

	1521		1600
shVEM_1_n.a.	-----CGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCC		
shVEM_2_n.a.			
shVEM_3_n.a.	CTTCTCTCCACCTCCCCATAGCCGAGCTTGGAAAAGTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCC		
mHVEM_2_n.a.	-----		
mHVEM_pub._n.a.	-----		
	1601		1680
shVEM_1_n.a.	AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC		
shVEM_2_n.a.	-----		
shVEM_3_n.a.	AGCCTCCCTGGGACCTGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGC		
mHVEM_2_n.a.	-----G-----		
mHVEM_pub._n.a.	-----G-----		
	1681		1760
shVEM_1_n.a.	TGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
shVEM_2_n.a.	-----		
shVEM_3_n.a.	TGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
mHVEM_2_n.a.	-----TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
mHVEM_pub._n.a.	-----TGCAGCTGGCTGGTGACGAAGGCCGGAGCTGGGACCAGC		
	1761		1840
shVEM_1_n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG		
shVEM_2_n.a.	-----TTG-----GCCTAATCATATG		
shVEM_3_n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG		
mHVEM_2_n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG		
mHVEM_pub._n.a.	AGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATG		
	1841		1920
shVEM_1_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCATC-----		
shVEM_2_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGA-GCA--CACGG---CGGCCCCATCAGGG-----CTCATGTCCCCAGCCG		
shVEM_3_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC-----		
mHVEM_2_n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTCAGGTATTGATCCTCCTCCCCCTCTCCC		
mHVEM_pub._n.a.	TGTGAAAAGAAGAAAGCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTC-----		
	1921		2000
shVEM_1_n.a.	-----		
shVEM_2_n.a.	TCACCTCTTGG-----AGCTCTG-TCACCCCAA---GCCTGG-----GAGGTGGC-CCCAGAGCTT		
shVEM_3_n.a.	-----		
mHVEM_2_n.a.	TCCCCCTCCACCTTCCACCTCCCCCTCTCCCCGCTGGGGCTGGTGTCTTCTGGTGACATGGTGGGGCTCCCAGTTCTC		
mHVEM_pub._n.a.	-----		
	2001		2080
shVEM_1_n.a.	-----		
shVEM_2_n.a.	TTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTG---CAGG-----CTGGG-GCAGG---		
shVEM_3_n.a.	-----		
mHVEM_2_n.a.	TG--AGGGTCCTGAG-TCTTTCAAGTACAGCCACGGTAGCTCAGGAAAGAACCACCCCTCAAAC TGAAAGCAGTAAAA		
mHVEM_pub._n.a.	-----		
	2081		2160
shVEM_1_n.a.	-----CAGCGGAAAAGACA		
shVEM_2_n.a.	TGA-----TG TAGTC--AAGG---TGATC-----G-TCTCCA-----TC-CAGCGGAAAAGACA		
shVEM_3_n.a.	-----CAGCGGAAAAGACA		
mHVEM_2_n.a.	TGAACCCGAGAACCTGGAGTCCCAGGGGGGCTGAGCAGGCAGGGTCTCCACGATTCTGTGCTCACAGCGGAAAAGACA		
mHVEM_pub._n.a.	-----CAGCGGAAAAGACA		
	2161		2240
shVEM_1_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
shVEM_2_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
shVEM_3_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
mHVEM_2_n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		
mHVEM_pub._n.a.	GGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAA		

Figure 9C

shVEM_1_n.a.	2241	2320
shVEM_2_n.a.	TACCCTCATTACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCCGACGCCAGAGATACCTGGAGCGACGG	
shVEM_3_n.a.	TACCCTCATTACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCCGACGCCAGAGATACCTGGAGCGACGG	
mHVEM_2_n.a.	TACCCTCATTACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCCGACGCCAGAGATACCTGGAGCGACGG	
mHVEM__pub.__n.a.	TACCCTCATTACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCCGACGCCAGAGATACCTGGAGCGACGG	
shVEM_1_n.a.	2321	2400
shVEM_2_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_3_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM_2_n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
mHVEM__pub.__n.a.	CTGCTGAAAGAGGCTGTCCACCTGGCGAAACCACCGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGCTTCCGTCT	
shVEM_1_n.a.	2401	2480
shVEM_2_n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
shVEM_3_n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
mHVEM_2_n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
mHVEM__pub.__n.a.	CCTCCAGTGGAGGGAGAGGTGGGGCCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAGGG	
shVEM_1_n.a.	2481	2560
shVEM_2_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
shVEM_3_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
mHVEM_2_n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
mHVEM__pub.__n.a.	CCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCTTGAGGAGGAGCGCCAGTTGCCCTCGCTCACAGACCA	
shVEM_1_n.a.	2561	2640
shVEM_2_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_3_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM_2_n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
mHVEM__pub.__n.a.	CACACCCAGCCCTCCTGGGCCAGCCCAGAGGGCCCTTCAGACCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCA	
shVEM_1_n.a.	2641	2720
shVEM_2_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
shVEM_3_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
mHVEM_2_n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
mHVEM__pub.__n.a.	GGACAGGCCCCGGGCACTGCCTCACAGCCAAGGCTGGACTGGGTGGCTGCAGTGTGGTGTGTTAGTGGATACACATCGG	
shVEM_1_n.a.	2721	2800
shVEM_2_n.a.	AAGTGATTTTCTAAATTGGATTGGAATTCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGTTGGGAGATGCTGTG	
shVEM_3_n.a.	AAGTGATTTTCTAAATTGGATTGGAATTCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGTTGGGAGATGCTGTG	
mHVEM_2_n.a.	AAGTGATTTTCTAAATTGGATTGGAATTCGGCTCCTGTTTTCTATTGTGTCATGAAACAGTGTATTGTTGGGAGATGCTGTG	
mHVEM__pub.__n.a.	AAGTGATTTTCTAAATTGGATTGGAATTCGGCTCCTGTTTCTATTGTGTCATGAAACAGTGTATTGTTGGGAGATGCTGTG	
shVEM_1_n.a.	2801	2880
shVEM_2_n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
shVEM_3_n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
mHVEM_2_n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
mHVEM__pub.__n.a.	GGAGGATGTAAATATCTTGTTTCTCCTCAA----	
shVEM_1_n.a.	2881	2904
shVEM_2_n.a.	-----	
shVEM_3_n.a.	-----GGGCGGCCGC	
mHVEM_2_n.a.	AAAAAAAAAAAAAAGGGCGGCCGC	
mHVEM__pub.__n.a.	-----	

Figure 9D

	1	80
shVEM_1_a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_2_a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
shVEM_3_a.a.	MEPPGDWGGPPWRSTPRTDVSRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM_2_a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
mHVEM__pub.__a.a.	MEPPGDWGGPPWRSTPRTDVLRLVLVLTFLGAPCYAPALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPP	
	81	160
shVEM_1_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_2_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
shVEM_3_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM_2_a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
mHVEM__pub.__a.a.	GTYYIAHLNGLSKCLQCQMCDPAMGLRASRNCsrTENAVCGCSPGHFCIVQGDHCAACRAYATSSPGQRVQKGGTESQDT	
	161	240
shVEM_1_a.a.	LCQNCPPGTFSPNGTLEECQHQTNRWKSQTDL-----	
shVEM_2_a.a.	LCQNCPPGTFSPNGTLEECQHQTNPWPNHMCCKKAKG-----	
shVEM_3_a.a.	LCQNCPPGTFSPNGTLEECQHQTCKA-----	
mHVEM_2_a.a.	LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHVWWFSLGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
mHVEM__pub.__a.a.	LCQNCPPGTFSPNGTLEECQHQTCKSWLVTKAGAGTSSSHVWWFSLGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVS	
	241	283
shVEM_1_a.a.	-----	
shVEM_2_a.a.	-----	
shVEM_3_a.a.	-----	
mHVEM_2_a.a.	VQVLILLPLSLPPPPSHLPSRWGWCFWCTWWGLPVL-----	
mHVEM__pub.__a.a.	VQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH	

Figure 10